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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/917,974

DATE: 08/17/2001

TIME: 06:10:34

Input Set : N:\Crf3\RULE60\09917974.txt

Output Set: N:\CRF3\08162001\I917974.raw

3 <110> APPLICANT: Ligensa, Tanja
4 Schumacher, Ralf
5 Weidner, Michael
7 <120> TITLE OF INVENTION: IGF-1 Receptor Interacting Proteins
9 <130> FILE REFERENCE: 09/453,195
11 <140> CURRENT APPLICATION NUMBER: 09/917,974
C--> 12 <141> CURRENT FILING DATE: 2001-07-30
14 <150> PRIOR APPLICATION NUMBER: 09/453,195
15 <151> PRIOR FILING DATE: 1999-12-02
17 <160> NUMBER OF SEQ ID NOS: 10
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1707
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <223> OTHER INFORMATION: n at position 186, 187, 203, and 205 is a, t, g, or c.
29 <400> SEQUENCE: 1
30 gaaacccaca ggaggaacc acactagttt agatcttctg gtgacccac ttctcgtgc 60
31 tcatgcecgct gggactgggg cggcgaaaa aggcgcccc tctagtggaa aatgaggagg 120
32 ctgagccagg ccgtggagg ctgggcgtgg gggagccagg gcctctgggc ggaggtgggt 180
W--> 33 cggggnnccc ccaaattgggc ttncncccc cccccagc cctgcggccc cgcctcgtgt 240
34 tccacaccca gctggcccat ggcagtccca ctggccgcat cgagggcttc accaacgtca 300
35 aggagctgta tggcaagatc gccgaggcct tccgcctgcc aactgccgag gtgatgttct 360
36 gcaccctgaa caccacaaaa gtggacatgg acaagctcct ggggggcccag atcgggctgg 420
37 aggatctcat ctctgcccac gtgaaggggc agcgcaagga ggtggagggtg ttcaagtcgg 480
38 aggatgcact cgggctcacc atcacggaca acggggctgg ctacgccttc atcaagcgca 540
39 tcaaggaggg cagcgtgatc gaccacatcc acctcatcag cgtgggcccag atgatcgagg 600
40 ccattaacgg gcagagcctg ctgggctgcc ggcactacga ggtggcccgg ctgctcaagg 660
41 agctgccccg aggcctgacc ttacgctga agctcacgga gcctcgcaag gccttcgaca 720
42 tgatcagcca gcgttcagcg ggtggccgcc ctggctctgg cccacaactg ggcactggcc 780
43 gagggaacct gcggctccga tcccggggcc ccgccacggt ggaggatctg cctctgcct 840
44 ttgaagagaa ggccattgag aagggtggatg acctgctgga gagttacatg ggtatcaggg 900
45 acacggagct ggcagccacc atggtggagc tgggaaagga caaaaggaa cccgatgagc 960
46 tggccgaggg cctggacgaa cggctgggtg actttgctt cctgacgag ttctgtttg 1020
47 acgtctgggg cgccattggg gacgccaagg tcggccgcta ctaggactgc ccccgaccc 1080
48 tgcgatgatg acccgggcgc aacctggtgg gggccccag cagggacact gacgtcagga 1140
49 cccgagcctc cagcctgagc ctagtccagc agcccaagga cgtatggtgag gggaggtggg 1200
50 gccaggcccc ctgccccgct ccactcggtg ccatccctc cctggttccc agtctggccg 1260
51 gggccccgg cccccctgtg cctgtttccc cacctacctc agctgggtca ggcacaggga 1320
52 ggggagggat cagccaaatt gggcgccacc cccgcctcc accactttcc accatcagct 1380
53 gccaaactgg tccctctgtc tccctggggc cttgggttct gtttgggggt catgaccttc 1440
54 ctagtctcct gacgcaggga atacaggga gagggtgtgc cttcccccca gcaaattgaa 1500
55 taatgccctc acccctcctg agaggagccc cctccctgtg gagcctgta cctccgcatt 1560
56 tgacacgagt ctgtgtgaa ccccgcaacc tctccccac ctcccatctc tcttccagg 1620
57 cccatccctg gccagagca ggaggaggg agggacgatg gcggtgggtt tttgtatctg 1680
58 aatttgcgtg cttgaacata aagaatc 1707

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61 <210> SEQ ID NO: 2

62 <211> LENGTH: 333

63 <212> TYPE: PRT

64 <213> ORGANISM: Homo sapiens

66 <220> FEATURE:

67 <223> OTHER INFORMATION: Xaa at position 42, 47, and 48 is any one of the twenty naturally

68 occurring amino acids.

70 <400> SEQUENCE: 2

71 Met Pro Leu Gly Leu Gly Arg Arg Lys Lys Ala Pro Pro Leu Val Glu
 72 1 5 10 15
 74 Asn Glu Glu Ala Glu Pro Gly Arg Gly Gly Leu Gly Val Gly Glu Pro
 75 20 25 30
 W--> 77 Gly Pro Leu Gly Gly Gly Ser Gly Xaa Pro Gln Met Gly Xaa Xaa
 78 35 40 45
 80 Pro Pro Pro Pro Ala Leu Arg Pro Arg Leu Val Phe His Thr Gln Leu
 81 50 55 60
 83 Ala His Gly Ser Pro Thr Gly Arg Ile Glu Gly Phe Thr Asn Val Lys
 84 65 70 75 80
 86 Glu Leu Tyr Gly Lys Ile Ala Glu Ala Phe Arg Leu Pro Thr Ala Glu
 87 85 90 95
 89 Val Met Phe Cys Thr Leu Asn Thr His Lys Val Asp Met Asp Lys Leu
 90 100 105 110
 92 Leu Gly Gly Gln Ile Gly Leu Glu Asp Phe Ile Phe Ala His Val Lys
 93 115 120 125
 95 Gly Gln Arg Lys Glu Val Glu Val Phe Lys Ser Glu Asp Ala Leu Gly
 96 130 135 140
 98 Leu Thr Ile Thr Asp Asn Gly Ala Gly Tyr Ala Phe Ile Lys Arg Ile
 99 145 150 155 160
 101 Lys Glu Gly Ser Val Ile Asp His Ile His Leu Ile Ser Val Gly Asp
 102 165 170 175
 104 Met Ile Glu Ala Ile Asn Gly Gln Ser Leu Leu Gly Cys Arg His Tyr
 105 180 185 190
 107 Glu Val Ala Arg Leu Leu Lys Glu Leu Pro Arg Gly Arg Thr Phe Thr
 108 195 200 205
 110 Leu Lys Leu Thr Glu Pro Arg Lys Ala Phe Asp Met Ile Ser Gln Arg
 111 210 215 220
 113 Ser Ala Gly Gly Arg Pro Gly Ser Gly Pro Gln Leu Gly Thr Gly Arg
 114 225 230 235 240
 116 Gly Thr Leu Arg Leu Arg Ser Arg Gly Pro Ala Thr Val Glu Asp Leu
 117 245 250 255
 119 Pro Ser Ala Phe Glu Glu Lys Ala Ile Glu Lys Val Asp Asp Leu Leu
 120 260 265 270
 122 Glu Ser Tyr Met Gly Ile Arg Asp Thr Glu Leu Ala Ala Thr Met Val
 123 275 280 285
 125 Glu Leu Gly Lys Asp Lys Arg Asn Pro Asp Glu Leu Ala Glu Ala Leu
 126 290 295 300
 128 Asp Glu Arg Leu Gly Asp Phe Ala Phe Pro Asp Glu Phe Val Phe Asp
 129 305 310 315 320
 131 Val Trp Gly Ala Ile Gly Asp Ala Lys Val Gly Arg Tyr

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132          325          330
135 <210> SEQ ID NO: 3
136 <211> LENGTH: 380
137 <212> TYPE: DNA
138 <213> ORGANISM: Homo sapiens
140 <220> FEATURE:
141 <223> OTHER INFORMATION: n at position 369 is a, t, g, or c.
143 <400> SEQUENCE: 3
144 gccgaggaag gagaaggggc taaaccttgg agagtggatg gctcaaagga ttctcagatc 60
145 acacctcggg aggatcatgg gcaggagagc ctgttggcag ggctccacgg aacgcatcca 120
146 ccaaagacaa ggcagaaagt cactgcccac gccggaggcc ccggggatcc catgcttttt 180
147 tcaagcccag agacagatga gaagcttttt atatgtgcgc agtgtggcaa aaccttcaac 240
148 aataacctcca acctgagaac gcaccagcgg atccacactg gcgagaagcc ctacatgtgt 300
149 tccgagtgtg gcaagagttt ctcccggagc tccaaccgca tccggcacga gcgcatccac 360
W--> 150 ctggaagana agcactctga 380
153 <210> SEQ ID NO: 4
154 <211> LENGTH: 126
155 <212> TYPE: PRT
156 <213> ORGANISM: Homo sapiens
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Xaa at position 123 is any one of the twenty naturally
occurring amino
160 acids.
162 <400> SEQUENCE: 4
163 Ala Glu Glu Gly Glu Gly Ala Lys Pro Trp Arg Val Asp Gly Ser Lys
164 1 5 10 15
166 Asp Ser Gln Ile Thr Pro Arg Glu Asp His Gly Gln Glu Ser Leu Leu
167 20 25 30
169 Ala Gly Leu His Gly Thr His Pro Lys Thr Arg Gln Lys Val Thr
170 35 40 45
172 Ala Gln Ala Gly Gly Pro Gly Asp Pro Met Leu Phe Ser Ser Pro Glu
173 50 55 60
175 Thr Asp Glu Lys Leu Phe Ile Cys Ala Gln Cys Gly Lys Thr Phe Asn
176 65 70 75 80
178 Asn Thr Ser Asn Leu Arg Thr His Gln Arg Ile His Thr Gly Glu Lys
179 85 90 95
181 Pro Tyr Met Cys Ser Glu Cys Gly Lys Ser Phe Ser Arg Ser Ser Asn
182 100 105 110
W--> 184 Arg Ile Arg His Glu Arg Ile His Leu Glu Xaa Lys His Ser
185 115 120 125
188 <210> SEQ ID NO: 5
189 <211> LENGTH: 678
190 <212> TYPE: DNA
191 <213> ORGANISM: Homo sapiens
193 <400> SEQUENCE: 5
194 atgtcgagac cccggaagag gctggctggg acttctggtt cagacaaggg actatcagga 60
195 aaacgcacca aaactgagaa ctcaggtgag gcattagcta aagtggagga ctccaaccct 120
196 cagaagactt cagccactaa aaactgtttg aagaatctaa gcagccactg gctgatgaag 180
197 tcagagccag agagccgcct agagaaaggt gtagatgtga agttcagcat tgaggatctc 240
198 aaagcacagc ccaaacagac aacatgctgg gatggtgttc gtaactacca ggctcggaa 300

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199 ttccttagag ccatgaagct gggagaagaa gccttcttct accatagcaa ctgcaaagag 360
200 ccaggcatcg caggactcat gaagatcgtg aaagaggctt acccagacca cacacagttt 420
201 gagaaaaaca atccccatta tgacccatct agcaaagagg acaaccctaa gtggtccatg 480
202 gtggatgtac agtttggtcg gatgatgaaa cgtttcattc ccctggctga gctcaaattcc 540
203 tatcatcaag ctacaaaagc tactggtggc cccttaaaaa atatggttct cttcactcgc 600
204 cagagattat caatccagcc cctgacccag gaagagtttg attttgtttt gagcctggag 660
205 gaaaaggaac caagttaa                                     678
208 <210> SEQ ID NO: 6
209 <211> LENGTH: 225
210 <212> TYPE: PRT
211 <213> ORGANISM: Homo sapiens
213 <400> SEQUENCE: 6
214 Met Ser Arg Pro Arg Lys Arg Leu Ala Gly Thr Ser Gly Ser Asp Lys
215 1 5 10 15
217 Gly Leu Ser Gly Lys Arg Thr Lys Thr Glu Asn Ser Gly Glu Ala Leu
218 20 25 30
220 Ala Lys Val Glu Asp Ser Asn Pro Gln Lys Thr Ser Ala Thr Lys Asn
221 35 40 45
223 Cys Leu Lys Asn Leu Ser Ser His Trp Leu Met Lys Ser Glu Pro Glu
224 50 55 60
226 Ser Arg Leu Glu Lys Gly Val Asp Val Lys Phe Ser Ile Glu Asp Leu
227 65 70 75 80
229 Lys Ala Gln Pro Lys Gln Thr Thr Cys Trp Asp Gly Val Arg Asn Tyr
230 85 90 95
232 Gln Ala Arg Asn Phe Leu Arg Ala Met Lys Leu Gly Glu Glu Ala Phe
233 100 105 110
235 Phe Tyr His Ser Asn Cys Lys Glu Pro Gly Ile Ala Gly Leu Met Lys
236 115 120 125
238 Ile Val Lys Glu Ala Tyr Pro Asp His Thr Gln Phe Glu Lys Asn Asn
239 130 135 140
241 Pro His Tyr Asp Pro Ser Ser Lys Glu Asp Asn Pro Lys Trp Ser Met
242 145 150 155 160
244 Val Asp Val Gln Phe Val Arg Met Met Lys Arg Phe Ile Pro Leu Ala
245 165 170 175
247 Glu Leu Lys Ser Tyr His Gln Ala His Lys Ala Thr Gly Gly Pro Leu
248 180 185 190
250 Lys Asn Met Val Leu Phe Thr Arg Gln Arg Leu Ser Ile Gln Pro Leu
251 195 200 205
253 Thr Gln Glu Glu Phe Asp Phe Val Leu Ser Leu Glu Glu Lys Glu Pro
254 210 215 220
256 Ser
257 225
260 <210> SEQ ID NO: 7
261 <211> LENGTH: 18
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence:primer TIP2c-s
268 <400> SEQUENCE: 7

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269 gaaacccaca ggaggcaa 18
272 <210> SEQ ID NO: 8
273 <211> LENGTH: 18
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Description of Artificial Sequence:primer TIP2b-r
280 <400> SEQUENCE: 8
281 ggtcatcatc gcagggtc 18
284 <210> SEQ ID NO: 9
285 <211> LENGTH: 33
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence:primer Hcthy-s
292 <400> SEQUENCE: 9
293 agcttgcggc cgcagatgtc gagaccccg aag 33
296 <210> SEQ ID NO: 10
297 <211> LENGTH: 40
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence:primer Hcthy-r
304 <400> SEQUENCE: 10
305 agcttgcggc cgcgaattct taacttggtt ccttttcctc 40
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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09917974.txt

Output Set: N:\CRF3\08162001\I917974.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:33 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:77 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:77 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:150 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:150 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:184 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:184 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4